

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: Lyman, Stewart D.  
Beckmann, M. Patricia
- (ii) TITLE OF INVENTION: Ligands for flt3 Receptors
- (iii) NUMBER OF SEQUENCES: 8
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Stephen L. Malaska, Immunex Corporation
  - (B) STREET: 51 University Street
  - (C) CITY: Seattle
  - (D) STATE: Washington
  - (E) COUNTRY: US
  - (F) ZIP: 98101
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: Apple Macintosh
  - (C) OPERATING SYSTEM: Macintosh 7.0.1
  - (D) SOFTWARE: Microsoft Word, Version #5.1
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: -to be assigned-
  - (B) FILING DATE: March 7, 1994
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: 08/162,407
  - (B) FILING DATE: December 3, 1993
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: 08/111,758
  - (B) FILING DATE: August 25, 1993
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: 08/106,463
  - (B) FILING DATE: August 12, 1993
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: 08/068,394
  - (B) FILING DATE: May 24, 1993
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Malaska, Stephen L.
  - (B) REGISTRATION NUMBER: 32,655
  - (C) REFERENCE/DOCKET NUMBER: 2813-D
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (206) 587-0430
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  - (C) TELEX: 756822

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 879 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 1..25

## (ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 855..879

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 57..752

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTCTGACTGGA	ACGAGACGAC	CTGCTCTGTC	ACAGGCATGA	GGGGTCCCCG	GCAGAG	56
ATG ACA GTG CTG GCG CCA GCC TGG AGC CCA AAT TCC TCC CTG TTG CTG	104					
Met Thr Val Leu Ala Pro Ala Trp Ser Pro Asn Ser Ser Leu Leu Leu						
1 5 10 15						
CTG TTG CTG CTG CTG AGT CCT TGC CTG CGG GGG ACA CCT GAC TGT TAC	152					
Leu Leu Leu Leu Leu Ser Pro Cys Leu Arg Gly Thr Pro Asp Cys Tyr						
20 25 30						
TTC AGC CAC AGT CCC ATC TCC TCC AAC TTC AAA GTG AAG TTT AGA GAG	200					
Phe Ser His Ser Pro Ile Ser Ser Asn Phe Lys Val Lys Phe Arg Glu						
35 40 45						
TTG ACT GAC CAC CTG CTT AAA GAT TAC CCA GTC ACT GTG GCC GTC AAT	248					
Leu Thr Asp His Leu Leu Lys Asp Tyr Pro Val Thr Val Ala Val Asn						
50 55 60						
CTT CAG GAC GAG AAG CAC TGC AAG GCC TTG TGG AGC CTC TTC CTA GCC	296					
Leu Gln Asp Glu Lys His Cys Lys Ala Leu Trp Ser Leu Phe Leu Ala						
65 70 75 80						
CAG CGC TGG ATA GAG CAA CTG AAG ACT GTG GCA GGG TCT AAG ATG CAA	344					
Gln Arg Trp Ile Glu Gln Leu Lys Thr Val Ala Gly Ser Lys Met Gln						
85 90 95						
ACG CTT CTG GAG GAC GTC AAC ACC GAG ATA CAT TTT GTC ACC TCA TGT	392					
Thr Leu Leu Glu Asp Val Asn Thr Glu Ile His Phe Val Thr Ser Cys						
100 105 110						

ACC	TTC	CAG	CCC	CTA	CCA	GAA	TGT	CTG	CGA	TTC	GTC	CAG	ACC	AAC	ATC	440									
Thr	Phe	Gln	Pro	Leu	Pro	Glu	Cys	Leu	Arg	Phe	Val	Gln	Thr	Asn	Ile										
		115					120					125													
TCC	CAC	CTC	CTG	AAG	GAC	ACC	TGC	ACA	CAG	CTG	CTT	GCT	CTG	AAG	CCC	488									
Ser	His	Leu	Leu	Lys	Asp	Thr	Cys	Thr	Gln	Leu	Leu	Ala	Leu	Lys	Pro										
		130					135					140													
TGT	ATC	GGG	AAG	GCC	TGC	CAG	AAT	TTC	TCT	CGG	TGC	CTG	GAG	GTG	CAG	536									
Cys	Ile	Gly	Lys	Ala	Cys	Gln	Asn	Phe	Ser	Arg	Cys	Leu	Glu	Val	Gln										
		145				150				155					160										
TGC	CAG	CCG	GAC	TCC	TCC	ACC	CTG	CTG	CCC	CCA	AGG	AGT	CCC	ATA	GCC	584									
Cys	Gln	Pro	Asp	Ser	Ser	Thr	Leu	Leu	Pro	Pro	Arg	Ser	Pro	Ile	Ala										
				165						170					175										
CTA	GAA	GCC	ACG	GAG	CTC	CCA	GAG	CCT	CGG	CCC	AGG	CAG	CTG	TTG	CTC	632									
Leu	Glu	Ala	Thr	Glu	Leu	Pro	Glu	Pro	Arg	Pro	Arg	Gln	Leu	Leu	Leu										
			180					185					190												
CTG	CTG	CTG	CTG	CTG	CCT	CTC	ACA	CTG	GTG	CTG	CTG	GCA	GCC	GCC	TGG	680									
Leu	Leu	Leu	Leu	Leu	Pro	Leu	Thr	Leu	Val	Leu	Leu	Ala	Ala	Ala	Trp										
			195				200					205													
GGC	CTT	CGC	TGG	CAA	AGG	GCA	AGA	AGG	AGG	GGG	GAG	CTC	CAC	CCT	GGG	728									
Gly	Leu	Arg	Trp	Gln	Arg	Ala	Arg	Arg	Arg	Gly	Glu	Leu	His	Pro	Gly										
		210				215					220														
GTG	CCC	CTC	CCC	TCC	CAT	CCC	TAGGATTCGA				GCCTTGTCGA				TCGTTGACTC		779								
Val	Pro	Leu	Pro	Ser	His	Pro																			
						230																			
AGCCAGGGTC TTATCTCGGT TACACCTGTA ATCTCAGCCC TTGGGAGCCC AGAGCAGGAT																839									
TGCTGAATGG TCTGGAGCAG GTCGTCTCGT TCCAGTCGAC																879									

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Thr	Val	Leu	Ala	Pro	Ala	Trp	Ser	Pro	Asn	Ser	Ser	Leu	Leu	Leu	
1				5					10					15		
Leu	Leu	Leu	Leu	Leu	Ser	Pro	Cys	Leu	Arg	Gly	Thr	Pro	Asp	Cys	Tyr	
			20					25					30			
Phe	Ser	His	Ser	Pro	Ile	Ser	Ser	Asn	Phe	Lys	Val	Lys	Phe	Arg	Glu	
		35					40					45				
Leu	Thr	Asp	His	Leu	Leu	Lys	Asp	Tyr	Pro	Val	Thr	Val	Ala	Val	Asn	
		50				55					60					

Leu Gln Asp Glu Lys His Cys Lys Ala Leu Trp Ser Leu Phe Leu Ala  
 65 70 75 80  
 Gln Arg Trp Ile Glu Gln Leu Lys Thr Val Ala Gly Ser Lys Met Gln  
 85 90 95  
 Thr Leu Leu Glu Asp Val Asn Thr Glu Ile His Phe Val Thr Ser Cys  
 100 105 110  
 Thr Phe Gln Pro Leu Pro Glu Cys Leu Arg Phe Val Gln Thr Asn Ile  
 115 120 125  
 Ser His Leu Leu Lys Asp Thr Cys Thr Gln Leu Leu Ala Leu Lys Pro  
 130 135 140  
 Cys Ile Gly Lys Ala Cys Gln Asn Phe Ser Arg Cys Leu Glu Val Gln  
 145 150 155 160  
 Cys Gln Pro Asp Ser Ser Thr Leu Leu Pro Pro Arg Ser Pro Ile Ala  
 165 170 175  
 Leu Glu Ala Thr Glu Leu Pro Glu Pro Arg Pro Arg Gln Leu Leu Leu  
 180 185 190  
 Leu Leu Leu Leu Leu Pro Leu Thr Leu Val Leu Leu Ala Ala Ala Trp  
 195 200 205  
 Gly Leu Arg Trp Gln Arg Ala Arg Arg Arg Gly Glu Leu His Pro Gly  
 210 215 220  
 Val Pro Leu Pro Ser His Pro  
 225 230

## (2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TCGACTGGAA CGAGACGACC TGCT

24

## (2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AGCAGGTCGT CTCGTTCCAG

20

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 988 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 30..734

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGGCCGGAAT TCCGGGGCCC CCGGCCGAA	ATG ACA GTG CTG GCG CCA GCC TGG	53
	Met Thr Val Leu Ala Pro Ala Trp	
	1 5	
AGC CCA ACA ACC TAT CTC CTC CTG CTG CTG CTG AGC TCG GGA CTC	101	
Ser Pro Thr Thr Tyr Leu Leu Leu Leu Leu Leu Ser Ser Gly Leu		
10 15 20		
AGT GGG ACC CAG GAC TGC TCC TTC CAA CAC AGC CCC ATC TCC TCC GAC	149	
Ser Gly Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp		
25 30 35 40		
TTC GCT GTC AAA ATC CGT GAG CTG TCT GAC TAC CTG CTT CAA GAT TAC	197	
Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr		
45 50 55		
CCA GTC ACC GTG GCC TCC AAC CTG CAG GAC GAG GAG CTC TGC GGG GGC	245	
Pro Val Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Gly		
60 65 70		
CTC TGG CGG CTG GTC CTG GCA CAG CGC TGG ATG GAG CGG CTC AAG ACT	293	
Leu Trp Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr		
75 80 85		
GTC GCT GGG TCC AAG ATG CAA GGC TTG CTG GAG CGC GTG AAC ACG GAG	341	
Val Ala Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu		
90 95 100		
ATA CAC TTT GTC ACC AAA TGT GCC TTT CAG CCC CCC CCC AGC TGT CTT	389	
Ile His Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys Leu		
105 110 115 120		

CGC TTC GTC CAG ACC AAC ATC TCC CGC CTC CTG CAG GAG ACC TCC GAG 437  
 Arg Phe Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu  
 125 130 135

CAG CTG GTG GCG CTG AAG CCC TGG ATC ACT CGC CAG AAC TTC TCC CGG 485  
 Gln Leu Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg  
 140 145 150

TGC CTG GAG CTG CAG TGT CAG CCC GAC TCC TCA ACC CTG CCA CCC CCA 533  
 Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Pro Pro Pro  
 155 160 165

5 TGG AGT CCC CGG CCC CTG GAG GCC ACA GCC CCG ACA GCC CCG CAG CCC 581  
 Trp Ser Pro Arg Pro Leu Glu Ala Thr Ala Pro Thr Ala Pro Gln Pro  
 170 175 180

CCT CTG CTC CTC CTA CTG CTG CTG CCC GTG GGC CTC CTG CTG CTG GCC 629  
 Pro Leu Leu Leu Leu Leu Leu Leu Pro Val Gly Leu Leu Leu Leu Ala  
 185 190 195 200

GCT GCC TGG TGC CTG CAC TGG CAG AGG ACG CGG CGG AGG ACA CCC CGC 677  
 Ala Ala Trp Cys Leu His Trp Gln Arg Thr Arg Arg Arg Thr Pro Arg  
 205 210 215

CCT GGG GAG CAG GTG CCC CCC GTC CCC AGT CCC CAG GAC CTG CTG CTT 725  
 Pro Gly Glu Gln Val Pro Pro Val Pro Ser Pro Gln Asp Leu Leu Leu  
 220 225 230

GTG GAG CAC TGACCTGGCC AAGGCCTCAT CCTGCGGAGC CTAAACAAC 774  
 Val Glu His  
 235

GCAGTGAGAC AGACATCTAT CATCCCATTT TACAGGGGAG GATACTGAGG CACACAGAGG 834

GGAGTCACCA GCCAGAGGAT GTATAGCCTG GACACAGAGG AAGTTGGCTA GAGGCCGGTC 894

CCTTCCTTGG GCCCCTCTCA TTCCCTCCCC AGAATGGAGG CAACGCCAGA ATCCAGCACC 954

GGCCCCATTT ACCCAACTCT GAACAAAGCC CCCG 988

## (2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Thr Val Leu Ala Pro Ala Trp Ser Pro Thr Thr Tyr Leu Leu Leu  
 1 5 10 15

Leu Leu Leu Leu Ser Ser Gly Leu Ser Gly Thr Gln Asp Cys Ser Phe  
 20 25 30

Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu  
                   35                                  40                                  45  
 Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu  
           50                                  55                                  60  
 Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln  
   65                                  70                                  75                                  80  
 Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly  
                   85                                  90                                  95  
 Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala  
                   100                                  105                                  110  
 Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser  
           115                                  120                                  125  
 Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp  
   130                                  135                                  140  
 Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro  
  145                                  150                                  155                                  160  
 Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala  
                   165                                  170                                  175  
 Thr Ala Pro Thr Ala Pro Gln Pro Pro Leu Leu Leu Leu Leu Leu Leu  
           180                                  185                                  190  
 Pro Val Gly Leu Leu Leu Leu Ala Ala Ala Trp Cys Leu His Trp Gln  
   195                                  200                                  205  
 Arg Thr Arg Arg Arg Thr Pro Arg Pro Gly Glu Gln Val Pro Pro Val  
  210                                  215                                  220  
 Pro Ser Pro Gln Asp Leu Leu Leu Val Glu His  
  225                                  230                                  235

## (2) INFORMATION FOR SEQ ID NO:7:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA to mRNA

## (iii) HYPOTHETICAL: NO

## (iv) ANTI-SENSE: NO

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AATTGGTACC TTTGGATAAA AGAGACTACA AGGACGACGA TGACAAGACA CCTGACTGTT 60  
 ACTTCAGCCA C 71

## (2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATATGGATCC CTACTGCCTG GGCCGAGGCT CTGGGAG

37